WEST Search History

09/920953

DATE: Monday, June 09, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR			
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L2	ribosom$ and protein$	22008	L2
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END OF SEARCH HISTORY

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Staub, Robin L.

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FILE LAST UPDATED: 8 Jun 2003 (20030608/ED)
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L4 18 L3 NOT 2003/PY

=> s l4 not 2002/py 1069093 2002/PY

L5 16 L4 NOT 2002/PY

=> d l5 1-16 bib ab

L5 ANSWER 1 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1999:161202 CAPLUS
DN 130:322123
TI Cloning of a higher plant elongation factor 2 cDNA: Expression of eEF2 and .alpha. subunit of eEF1B in sugar beet cells during phosphate and carbohydrate starvation
AU Vogel, Rolf; Viereck, Ruth; Murmann, Andrea; Rausch, Thomas
CS Botanisches Institut, Ruprecht-Karls-Universitaet, Heidelberg, D-69120, Germany
SO Journal of Plant Physiology (1999), 154(2), 192-196 CODEN: JPPHEY; ISSN: 0176-1617

PB Urban & Fischer Verlag
DT Journal
LA English
AB In ribosomal protein synthesis of higher plants, the peptide elongation step depends, like in other eukaryotic and prokaryotic organisms, on several elongation factors, i.e. eEF1A, eEF1B (composed of three subunits; .alpha., .beta., .gamma.) and eEF2. We have isolated a full-length cDNA clone for eEF2 from sugar beet. The eEF2 protein sequence as predicted from the cDNA shows highest homol. with eEF2 from Chlorella kessleri, but is also highly similar to other eukaryotic eEF2s. We have analyzed the transcript amts. for eEF1B (.alpha.-subunit) and eEF2 in phosphate- and carbohydrate-starved sugar beet suspension-cultured cells and compared them with the transcript levels present in exponentially growing cells. Phosphate starvation affected growth but not the expression of both elongation factors. The dramatic decrease of eEF2 mRNA in response to carbohydrate starvation indicates that eEF2 expression is more sensitive towards nutrient depletion than expression of the eEF1B .alpha.-subunit.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1997:357772 CAPLUS
DN 127:76742
TI Complete nucleotide sequence of the chloroplast genome from the green alga Chlorella vulgaris: The existence of genes possibly involved in chloroplast division
AU Wakasugi, Tatsuya; Nagai, Toshiyuki; Kapoor, Meenu; Sugita, Mamoru; Ito, Mari; Ito, Shiho; Tsudzuki, Junko; Nakashima, Keiko; Tsudzuki, Takahiko; Suzuki, Yasuhiko; Hamada, Akira; Ohta, tutomu; Inamura, Atsushi; Yoshinaga, Koichi; Sugiura, Masahiro
CS Cent. Gene Res., Nagoya Univ., Nagoya, 464-01, Japan
SO Proceedings of the National Academy of Sciences of the United States of America (1997), 94(11), 5967-5972 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The complete nucleotide sequence of the chloroplast genome (150,613 bp) from the unicellular green alga Chlorella vulgaris C-27 was detd. The genome contains no large inverted repeat and has one copy of rRNA gene cluster consisting of 16S, 23S, and 5S rRNA genes. It contains 31 tRNA genes, of which the tRNALeu(GAG) gene has not been found in land plant chloroplast DNAs analyzed so far. Sixty-nine protein genes and 8 ORFs conserved with those found in land plant chloroplasts have also been found. The most striking is the existence of 2 adjacent genes homologous to bacterial genes involved in cell division, minD and minE, which are arranged in the same order in Escherichia coli. This finding suggests that the mechanism of chloroplast division is similar to bacterial division. Other than minD and minE homologs, genes encoding ribosomal proteins L5, L12, L19, and S9 (rpl5, rpl12, rpl19, and rps9); a chlorophyll biosynthesis Mg chelating subunit (chlI); and elongation factor EF-Tu (tufA), which have not been reported from land plant chloroplast DNAs, are present in this genome. However, many of the new chloroplast genes recently found in red and brown algae have not been found in C. vulgaris. Furthermore, this algal species possesses two long ORFs related to ycf1 and ycf2 that are exclusively found in land plants. These observations suggest that C. vulgaris is closer to land plants than to red and brown algae.

L5 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1995:771459 CAPLUS
DN 123:308930
TI Translation elongation factor-3 (EF-3): an evolving eukaryotic ribosomal protein ?
AU Belfield, G. P.; Ross-Smith, N. J.; Tuite, M. F.
CS Research School of Biosciences, Univ. of Kent, Kent, CT2 7NJ, UK
SO Journal of Molecular Evolution (1995), 41(3), 376-87 CODEN: JMEVAU; ISSN: 0022-2844
PB Springer
DT Journal
LA English
AB Fungi appear to be unique in their requirement for a third sol. translation elongation factor. This factor, designated elongation factor 3 (EF-3), exhibits ribosome-dependent ATPase and GTPase activities that are not intrinsic to the fungal ribosome but are nevertheless essential for translation elongation in vivo. The EF-3 polypeptide has been identified in a wide range of fungal species and the gene encoding EF-3 (YEF3) has been isolated from four fungal species (Saccharomyces cerevisiae, Candida albicans, Candida guillermondii, and Pneumocystis carinii). Computer-assisted anal. of the predicted S. cerevisiae EF-3 amino acid sequence was used to identify several potential functional domains; two ATP binding/catalytic domains conserved with equiv. domains in members of the ATP-Binding Cassette (ABC) family of proteins, an N-terminal region showing significant similarity to the Escherichia coli S5 ribosomal protein , and regions of predicted interaction with rRNA, tRNA, and mRNA. Furthermore, EF-3 was also found to display amino acid similarity to myosin proteins whose cellular function is to provide the motive force of muscle. The identification of these regions provides clues to both the evolution and function of EF-3. The predicted functional regions are conserved among all known fungal EF-3 proteins and recently described homolog encoded by the Chlorella virus CVK2. EF-3 may play a role in the ribosomal optimization of the accuracy of fungal protein synthesis by altering the conformation and activity of a ribosomal "accuracy center," which is equiv. to the S4-S5-S12 ribosomal protein accuracy center domain of the E. coli ribosome. Furthermore, EF-3 may represent an evolving ribosomal protein with properties analogous to the intrinsic ATPase activities of higher eukaryotic ribosomes, which has wider implications for the evolutionary divergence of fungi from other eukaryotes.

L5 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1993:250468 CAPLUS
DN 118:250468
TI Nucleotide sequence of the genes for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit and ribosomal protein S14 from a Chlorella -like green alga
AU Amberg, Sean M.; Meints, Russel H.
CS Cent. Gene Res. Biotechnol., Oregon State Univ., Corvallis, OR, 97331-2906, USA
SO Journal of Phycology (1991), 27(6), 753-8 CODEN: JPYLAJ; ISSN: 0022-3646
DT Journal
LA English
AB Two chloroplast genes were sequenced from an exsymbiotic strain of a eukaryotic, Chlorella -like green alga. The genes for the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcL) and the ribosomal protein S14 (rps14) were oriented in the same direction and were sepd. by 402 bp. The rbcLs of the exsymbiont and a free-living Chlorella ellipsoidea were compared with other reported rbcL sequences. The rbcL gene of the exsymbiont is closely related to that of free-living Chlorella ellipsoidea. This is the first published report of an rps14 gene sequence from an alga.

L5 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1980:441162 CAPLUS
DN 93:41162
TI Comparative electrophoretic study on ribosomal proteins from algae
AU Goetz, Helmut; Arnold, Carl Gerold
CS Inst. Bot. Pharm. Biol., Univ. Erlangen-Nuernberg, Erlangen, D-8520, Fed. Rep. Ger.
SO Planta (1980), 149(1), 19-26 CODEN: PLANAB; ISSN: 0032-0935
DT Journal
LA English
AB The proteins from cytoplasmic ribosomal subunits of 8 species of algae were analyzed by 2-dimensional gel electrophoresis. The mol. wts. of the proteins were in the range of 10,000 to 55,000. The protein patterns from the ribosomal subunits of the different species were compared to those of Chlamydomonas reinhardii. Many similarities in the protein patterns of all the investigated species were obsd.; for C. eugametos 48, C. noctigama 42, Chlorogonium elongatum 47, Scenedesmus obliquus 40, Chlorella fusca 35, and Euglena gracilis 35 proteins were homologous to those of C. reinhardii. For the colorless flagellate Polytoma papillatum, 45 proteins homologous to C. reinhardii were detected, so that the generally assumed close relation between Chalamydomonas and Polytoma is confirmed.

L5 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1980:71363 CAPLUS
DN 92:71363
TI Analysis of ribosomal proteins from various species of algae. II. Comparative electrophoretic study on proteins from chloroplast ribosomes
AU Goetz, Helmut; Arnold, Carl Gerold
CS Inst. Bot. Pharm. Biol., Univ. Erlangen-Nuernberg, Erlangen, Fed. Rep. Ger.
SO Biochemie und Physiologie der Pflanzen (1980), 175(1), 1-8 CODEN: BPPFA4; ISSN: 0015-3796
DT Journal
LA English
AB The proteins from chloroplast ribosomal subunits of 7 species of algae were characterized by 2-dimensional gel electrophoresis. The protein patterns from the chloroplast ribosomal subunits were compared to those of Chlamydomonas reinhardii. A high degree of evolutionary conservation was found among the ribosomal proteins of the different species. For C. eugametos, 26, C. noctigama, 27, Chlorogonium elongatum, 30, Scenedesmus obliquus, 25, and Euglena gracilis, 18 proteins were homologous to corresponding proteins in C. reinhardii. On the whole, the chloroplast ribosomal protein patterns differed slightly more on av. than the cytoplasmic ribosomal protein patterns of these species. No homologies were detected between chloroplast and cytoplasmic ribosomal proteins of the same species.

L5 ANSWER 7 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1977:185701 CAPLUS
DN 86:185701
TI Blue light-dependent regulation of cytoplasmic ribosomal RNA synthesis in Chlorella
AU Steup, Martin
CS Pflanzenphysiol. Inst., Univ. Goettingen, Goettingen, Fed. Rep. Ger.
SO Archives of Microbiology (1977), 112(3), 277-82 CODEN: AMICCW; ISSN: 0302-8933
DT Journal
LA English
AB The effects of blue and red light on ribosomal RNA synthesis in autotrophic synchronous cultures of C. pyrenoidosa (strain 211-8b) were studied by pulse labeling expts. with tritiated guanosine. Nucleic acids were sepd. by electrophoresis on polyacrylamide gels. Compd. with darkness and red light (679 nm), blue light (457 nm) of equal quantum flux stimulates incorporation into ribosomal RNA. This blue light effect was obsd. in the cytoplasmic ribosomal RNA after 5 min of illumination, whereas the stimulation of chloroplast ribosomal RNA synthesis by blue light appeared later. Maturation of chloroplast ribosomal RNA is slower than that of cytoplasmic ribosomal RNA. The blue light effect on the cytoplasmic ribosomal RNA formation does not require chloroplast RNA or protein synthesis. The blocking of cytoplasmic protein synthesis by cycloheximide inhibits the blue light effect on ribosomal RNA formation. It is concluded that the cytoplasmic ribosomal RNA transcription is controlled by a blue light sensitive sytem.

L5 ANSWER 8 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1975:603417 CAPLUS
DN 83:203417
TI Analysis of ribosomes by polyacrylamide gel electrophoresis
AU Ledoigt, Gerard; Curgy, Jean J.; Stevens, Barbara J.; Andre, Jean
CS Lab. Biol. Cellulaire, Univ. Paris XI, Orsay, Fr.
SO Biochimica et Biophysica Acta (1975), 407(2), 222-39 CODEN: BBACAQ; ISSN: 0006-3002
DT Journal
LA French
AB Ribosomal polymers, monomers, and subunits from several eukaryotes and prokaryotes were isolated and analyzed by polyacrylamide gel electrophoresis. Extn. of RNA from ribosomal particles after their migration in a polyacrylamide gel, analyses by sedimentation in sucrose gradients, and observations in the electron microscope were carried out in parallel. Attention was directed to the reproducibility, the precision, and the limitations of the electrophoresis technique. Electrophoresis of ribosomal particles produced narrow and well sepd. bands. This technique could characterize ribosomal particles and identify the particles in a mixt. (pellets, co-migration). The electrophoretic behavior of ribosomal particles was greatly dependent on their size and their spatial configuration. A systematic variation of the migration conditions demonstrated the following facts: the particles traveled distances proportional to the time of the migration, so that the resolving power increased as a function of time; the migration of the particles was inversely proportional to the square root of the acrylamide concn. and to the cationic concn. of the buffer (Na+, Mg2+); the clearest sepns. obtained were at .apprx.pH 8; and, when different prokaryotic particles or different eukaryotic particles were compared it was found that a log relation existed between the migration rate of the particles and their sedimentation coeffs. With an equiv. sedimentation coeff., a prokaryotic particle moved more rapidly than a eukaryotic particle. This phenomenon, along with several others (for prokaryotes, dissocn. in 2mM Mg2+, instability in the presence of EDTA and a heterogeneity of monomers and of their subunits) led to the conclusion that the 2 ribosomal types, 70 S and 80 S, have different conformations. Due to their very slow migration, mitochondrial ribosomes from Tetrahymena pyriformis appear to belong to a 3rd type. The migration rates of these 3 ribosomal types could be correlated with their resp. protein /RNA ratios.

L5 ANSWER 9 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1974:459627 CAPLUS
DN 81:59627
TI Comparative study of ribosomal proteins of blue-green algae and chloroplasts

AU Yurina, N. P.; Odintsova, M. S.
CS A. N. Bakh Inst. Biochem., Moscow, USSR
SO Biokhimiya (Moscow) (1974), 39(2), 348-58 CODEN: BIOHAO; ISSN: 0320-9725
DT Journal
LA Russian
AB Ribosomes from 5 species of blue-green algae, chloroplasts of the green alga Chlorella pyrenoidosa, and higher plants (pisum sativum and Chenopodium album) were studied by chem. and physicochem. methods. Polyacrylamide gel disc electrophoresis revealed possible phylogenetic relations between plastids and blue-green algae and between groups of Cyanophyta. The ribosomes of blue-green algae had a d. 1.61-1.64 and an RNA/protein ratio of 1.7. In cytoplasmic ribosomes of Chlorella and higher plants, the RNA/protein ratio was .apprx.1.0 (d. 1.55-1.56). Ribosomes of chloroplasts and blue-green algae differed in their RNA/protein ratios. Basic proteins of the unicellular Anacystis nidulans and Synechocystis aquatilis were less similar to each other than basic proteins of ribosomes of multicellular blue-green algae (Lyngbya species, Anabaena variabilis, Plectonema boryanum). The greatest similarity was noted for ribosomal proteins of the closely related species A. variabilis and P. boryanum. Ribosomes of chloroplasts differed from ribosomes of cytoplasm of the same species in the no. of protein components. Basic proteins of chloroplast ribosomes of higher plants were more similar to each other than to the ribosomal proteins of algae chloroplasts. In higher plants, interspecies differences in the protein compn. of ribosomes were greater in chloroplasts than in cytoplasm.

L5 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1973:144408 CAPLUS
DN 78:144408
TI Interaction between Escherichia coli ribosomal proteins and 5S RNA molecules. Recognition of prokaryotic 5S RNA and rejection of eukaryotic 5S RNA
AU Bellemare, G.; Vigne, R.; Jordan, B. R.
CS CBM/CNRS, Marseilles, Fr.
SO Biochimie (1973), 55(1), 29-35 CODEN: BICMBE; ISSN: 0300-9084
DT Journal
LA English
AB A specific binding test (incorporation into E. coli ribosomal subunits reconstituted from Li cores and Li supernatant) was used to assay the degree of structural homology between 5S RNA mols. from different origins. The 2 prokaryotic mols. tested are recognized to some extent by the system, but none of the 6 eukaryotic 5S RNAs tested can be incorporated into reconstituted subunits.

L5 ANSWER 11 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1972:963 CAPLUS
DN 76:963
TI Protein composition of ribosomes and sarcoma M-1 ribosome protein metabolism
AU Votrin, I. I.; Shishkin, S. S.; Debov, S. S.; Chernov, V. A.
CS Dep. Biochem., Moscow Med. Inst., Moscow, USSR
SO Biokhimiya (Moscow) (1971), 36(4), 752-60 CODEN: BIOHAO; ISSN: 0320-9725
DT Journal
LA Russian
AB Ribosome proteins of rat liver and sarcoma M-1 were extd. with HOAc and fractionated by electrophoresis in polyacrylamide gel. Electrophoregrams of both protein mixts. consisted of 6-7 intensely stained bands and differed in a no. of less intensely stained ones. Isoelec. focusing on Ampholine columns between pH values of 3 to 10 and 3 to 6 demonstrated slight differences in various protein fractions from both sources. Metabolic studies using 14C-labeled amino acids (hydrolyzate of Chlorella proteins) and leucine-14C have shown differences in the metabolic rates of the various protein fractions.

L5 ANSWER 12 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1971:431723 CAPLUS
DN 75:31723
TI Ribosome specificity of transfer factors from unicellular algae
AU Parisi, Bruno; Perani, A.; Tiboni, O.; Ciferri, Orio
CS Ist. Genet., Univ. Pavia, Pavia, Italy
SO Giornale Botanico Italiano (1970), 104(4), 277-87 CODEN: GBOIAX; ISSN: 0017-0070
DT Journal
LA English
AB The ribosome specificity of polymg. enzymes (contg. transfer factors) was detd. by in vitro assay of poly U-directed polyphenylalanine synthesis on either 70S (from Escherichia coli) or 80S (from Saccharomyces cerevisiae) ribosomes. In the prokaryote Nostoc muscorum, which contained only 70S ribosomes, the polymg. enzymes were active only on 70S ribosomes. Different patterns were obsd. in eukaryotes. Thus, polymg. enzymes from photosynthetic Euglena gracilis (contg. both (0S and 80S ribosomes) and photosynthetic Chlorella vulgaris (contg. only 80S ribosomes) are active on both 70S and 80S ribosomes. In dark-grown or achloric Euglena gracilis, the polymg. enzymes are active only on 80S ribosomes, but activity on 70S ribosomes was restored either by exposure to light, or by addn. of Escherichia coli transfer factor T. However, in nonphotosynthetic C. vulgaris and achloric P rototheca zopfii (contg. only 80S ribosomes), these enzymes are active on both 70S and 80S ribosomes. It is suggested that differences in the distributions of ribosomal types and polymg. enzymes contg. transfer factors may reflect a different degree of genetic and metabolic autonomy of the photosynthetic app. and (or) the chloroplast system for protein synthesis.

L5 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1967:418825 CAPLUS
DN 67:18825
TI Ribonucleic acids appearing during the process of chloroplast regeneration in the "glucose-bleached" cells of Chlorella protothecoides
AU Aoki, Shigeji; Hase, Eiji
CS Univ. Tokyo, Tokyo, Japan
SO Plant and Cell Physiology (1967), 8(1), 181-95 CODEN: PCPHA5; ISSN: 0032-0781
DT Journal
LA English
AB The modes of synthesis of different RNA species during greening (chloroplast regeneration) of glucose-bleached (chlorophyll (I)-less) cells of the alga, C. protothecoides, contg. markedly degenerated plastids was studied. During greening, the elution profiles of RNAs, in terms of absorbance at 260 m.mu. and of 32P, changed markedly. The synthesis of RNA, as well as that of sRNA, ceased around the 24th hr., and the amts. of RNAs, esp. rRNA, thereafter decreased. Both rRNA I and rRNA II were formed more actively than sRNA during the initial 8-hr. period, but these 2 species thereafter were biosynthesized (and partly degraded later) at a const. proportion. A high sRNA/rRNA ratio observed with the glucose-bleached cells may be an indication of the "resting" state of the algal cells. It appeared that rRNA III corresponded to the major component of the chloroplast rRNAs, and rRNA II to that of the "cytoplasmic" rRNAs. rRNA I was probably a mixt. of the minor components of the chloroplast and "cytoplasmic" rRNAs. The major events occurring in the early phase of chloroplast regeneration in glucosebleached cells

appeared to be ribosome formation in the plastid as well as in the cytoplasm. New ribosomal protein in the greening algal cells was probably synthesized later than the ribosomal RNA, and the findings suggested that the formation of chloroplast ribosomes was accelerated by light, and that ribosomal RNAs, esp. the chloroplast ribosomal RNA, undergo a degradation during the later phase of chloroplast regeneration, in which active formation of chlorophyll and protein continues.

L5 ANSWER 14 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1967:8954 CAPLUS
DN 66:8954
TI Sequential synthesis of ribosomal proteins in Escherichia coli K12 Ya-2 during the recovery from methionine starvation
AU Kamiryo, Tatsuyuki; Takagi, Masamichi; Maruo, Bunji
CS Univ. Tokyo, Tokyo, Japan
SO Journal of Biochemistry (Tokyo, Japan) (1966), 60(5), 602-4
CODEN: JOBIAO; ISSN: 0021-924X
DT Journal
LA English
AB Ribosomal proteins synthesized during recovery of E. coli cells from methionine starvation were labeled with 14C-labeled Chlorella protein hydrolyzate during the 5, 5-10, and 10-20 min. after methionine addn. to the starved cells. The pattern of relative specific activity of proteins labeled during the 1st 5 min. after methionine recovery differed from that of proteins labeled for 5 min. in the middle of the logarithmic growth phase of unstarved cells. There was no period in which the proteins of the 1st to the 4th fractions (obtained by disk electrophoresis in polyacrylamide gel) were preferentially synthesized during 20 min. of methionine recovery; when electrophoretic fractions 5 to 12 were considered, the less basic or the smaller the ribosomal proteins , the earlier were they synthesized during methionine recovery. The sum of the ribosomal proteins synthesized during the recovery roughly corresponded to the proteins of the normal ribosomes, except in the 1st-4th fractions. During the recovery period, the RNA-rich particles were converted to normal ribosomes; these particles probably combined with the newly synthesized ribosomal proteins and were converted into normal ribosomes during the 20-min. recovery period.

L5 ANSWER 15 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1966:105996 CAPLUS
DN 64:105996
OREF 64:20041a-c
TI Intracellular site of epidermal keratin synthesis
AU Priestley, G. C.; Speakman, P. T.
CS Univ. Leeds, UK
SO Nature (London, United Kingdom) (1966), 209(5030), 1336-7
CODEN: NATUAS; ISSN: 0028-0836
DT Journal
LA English
AB Fibrous proteins, usually involving more than one protein and each in a specific configuration and in a definite position with respect to the others, probably acquire their native structure at the time of synthesis and do not spontaneously assume their native three-dimensional arrangement after their synthesis. Native structure of fibrous proteins may arise as a result of concurrent synthesis of more than one polypeptide chain at large ribonucleoprotein complexes, which can be disrupted by proteolytic enzymes but not by RNases. Expts. were designed to discover the intracellular machinery which synthesizes epidermal keratin and perhaps gives it its native structure. Skin of the ventral surface of the sheep's ear, free from hair follicles, was used. The epidermis was trypsinized, homogenized, and centrifuged and the supernatant was fractionated by ultracentrifugation into a lipid layer, epidermal macro-mols., proteins , nucleic acids, ribosomes, and ribosomal subunits. The sedimentation coeff. of 74 S was typical for mammalian ribosomes. Epidermis was also used for incorporation expts. with 30 .mu.c. 14C-labeled amino acids from a protein hydrolyzate of Chlorella vulgaris. Incorporation was stopped after 1 min., the prepn. was homogenized and fractionated by sucrose density-gradient centrifugation, and the absorbance was measured at 260 m.mu.. RNase was used with some prepns. The Cl3CCO2H ppt. (protein) was filtered and the radioactivity of each fraction was measured. Single ribosomes had no radioactivity. There were no small polyribosomal aggregates, which are usually found in rapidly dividing cells or in cells synthesizing small protein mols. RNase had no effect on results. Thus, fibrous proteins of muscle and collagen were apparently synthesized at large ribonucleoprotein complexes, not at small ribosomal sites. 16 references.

L5 ANSWER 16 OF 16 CAPLUS COPYRIGHT 2003 ACS
AN 1965:31417 CAPLUS
DN 62:31417
OREF 62:5595g-h,5596a
TI Character and function of ribosomes from 8-azaguanine-treated cells of Bacillus cereus
AU Gruenberger, D.
CS Ceskoslov. Akad. Ved, Prague
SO Collection of Czechoslovak Chemical Communications (1965), 30(1), 128-37 CODEN: CCCCAK; ISSN: 0010-0765
DT Journal
LA English
AB The ribosomal fraction of a B. cereus culture that had been incubated with 25 .gamma. 8-azaguanine (I)/ml. incorporated I mainly into sol. RNA and a new ribosome component having a sedimentation coeff. between 30 and 4 S upon sucrose-gradient centrifugation. A cell-free ext. of B. cereus grown in 10-3M Mg++ without I, incorporated amino acids from a Chlorella 14C-tagged hydrolyzate and accumulated the radioactive peptides mainly in the 70 S and a part in the 100 S ribosomes; most of the ribosomes dissocd. to 50 S and 30 S fractions. In cell-free exts. of I-treated cultures, the incorporation was mainly in the 70 S ribosomes but was higher in the 30 S fraction than in the untreated microorganism. At a concn. 5 .times. 10-5M Mg++ the radioactivity passed for the most part into the supernatant fraction and in a lesser part into the 50 S ribosomes, rather than into the 30 S ribosomes. The ratio between the labeled amino acids incorporated into the ribosomal proteins and supernatant was about 2:1 in the microsomal system of normal cells and changed to approx. 4:1 in the ribosomes of cultures that had been grown in the presence of I.

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